

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description
1	483	29.5	298	1	JAM2_HUMAN	P57087 homo sapien
2	449.5	27.5	300	1	JAM1_MOUSE	088792 mus musculus
3	419	25.6	299	1	JAM1_HUMAN	09Y624 homo sapien
4	403.5	24.7	298	1	JAM1_BOVIN	09xt56 bos taurus
5	231.5	14.2	319	1	A33_HUMAN	09Y795 homo sapien
6	186	11.4	1088	1	NCA1_XENLA	P16170 xenopus laevis
7	180	11.0	333	1	ANBL_DROME	P15364 drosophila
8	177	10.8	1092	1	NCA2_XENLA	P36335 xenopus laevis
9	171.5	10.5	725	1	NCA2_MOUSE	P13594 mus musculus
10	171.5	10.5	1115	1	NCA2_MOUSE	P13595 mus musculus
11	171	10.5	1377	1	NBO1_RAT	P97603 rattus norvegicus
12	170.5	10.4	858	1	NCA1_RAT	P13596 rattus norvegicus
13	169.5	10.4	1912	1	PIPD_HUMAN	P23468 homo sapien
14	165	10.1	837	1	NCM2_HUMAN	015394 homo sapien
15	164.5	10.1	1051	1	PTK7_CHICK	Q91048 gallus gallus
16	164.5	10.1	3707	1	PGBM_MOUSE	005793 mus musculus
17	164	10.0	837	1	NCM2_MOUSE	035136 mus musculus
18	163.5	10.0	853	1	NCA1_BOVIN	P31836 bos taurus
19	163	10.0	1493	1	NBO1_MOUSE	P97798 mus musculus
20	162.5	9.9	6632	1	UNR99_CABEL	001761 caenorhabditis elegans
21	161.5	9.9	365	1	CXAR_HUMAN	P78310 homo sapien
22	158	9.7	1091	1	NCA1_CHICK	P13590 gallus gallus
23	155.5	9.5	761	1	NCA2_HUMAN	P13592 homo sapien
24	155.5	9.5	848	1	NCA1_HUMAN	P13591 homo sapien
25	155.5	9.5	1284	1	NRCA_CHICK	P35331 gallus gallus
26	153.5	9.4	1461	1	NEO1_HUMAN	Q92859 homo sapien
27	153	9.4	344	1	NTR1_HUMAN	Q9P121 homo sapien
28	151.5	9.3	349	1	LACH_SCHAM	Q26474 schistocerca gregaria
29	151	9.2	353	1	CEBU_CHICK	Q90773 gallus gallus
30	150.5	9.2	702	1	CEAS_HUMAN	P06731 homo sapien
31	149.5	9.1	1897	1	P10586_HUMAN	P10586 homo sapien
32	149	9.1	338	1	LAMP_CHICK	Q98919 gallus gallus
33	148.5	9.1	338	1	LAMP_RAT	Q62813 rattus norvegicus

ALIGNMENTS

RESULT 1	JAM2_HUMAN	STANDARD;	PRT;	298 AA.
ID	JAM2_HUMAN			
AC	P57087;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Junctional adhesion molecule 2 precursor (Vascular endothelial junction-associated molecule 2 precursor) (VE-JAM).			
GN	JAM2 OR VEJAM OR C21ORF43.			
RN	[1]			
SEQUENCE FROM N.A.				
RC	TISSUE=Vascular endothelial cells;			
RX	Medline=20317114; PubMed=1079521;			
RA	Palmezi D., van Zante A., Huang C.C., Hemmerich S., Rosen S.D.;			
RT	"Vascular endothelial junction-associated molecule, a novel member of the immunoglobulin superfamily, is localized to intercellular boundaries of endothelial cells."			
RT	Cunningham S.A., Arrate M.P., Rodriguez J.M., Bjerke R.J.,			
RL	J. Biol. Chem. 275:19139-19145(2000).			
RL	[2]			
SEQUENCE FROM N.A.				
RP				
RC				
RX				
RA				
RT				
RA	Vanderslice P., Morris A.P., Brock T.A.;			
RT	"A novel protein with homology to the junctional adhesion molecule: Characterization of leucocyte intercellular junctions."			
RL	J. Biol. Chem. 275:34750-34756(2000).			
RL	[3]			
SEQUENCE FROM N.A.				
RP				
RC	TISSUE=Lung;			
RX	Medline=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Shuemann C.M., Schuler G.D., Scheetz T.E.,			
RA	Klausner R.D., Collins F.S., Wagner L., Buetow K.H., Schaefer C.F., Bhat N.K., Altenschul S.P., Zeiberg B., Buetow K.H., Wang J., Hsieh F., Hopkins R.F., Jordan H., Moore T., Max S.I., Varnai P.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulahay S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grindwood J.J., Schmitz J., Myers R.M., Butfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E., Jones S.J.M., Marras M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			

CC -!- FUNCTION: MAY PLAY A ROLE IN THE PROCESSES OF LYMPHOCYTE HOMING TO
 CC -!- SECNDARY LYMPHOID ORGANS; TYPE I membrane protein (Potential)
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential)
 CC -!- TISSUE SPECIFICITY: PROMINENTLY EXPRESSED ON HIGH ENDOTHELIAL
 CC VENULES BUT IS ALSO PRESENT ON THE ENDOTHELIUM OF OTHER VESSELS.
 CC LOCALIZED TO THE INTERCELLULAR BOUNDARIES OF HIGH ENDOTHELIAL
 CC CELLS.
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like v-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- DATABASE: NAME=PROW; VERSION=2.1-3 (2001);
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/guide/1652492186_g.htm".
 CC -----
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 CC -----
 DR EMBL; AP255910; AAF81223.1; -.
 DR EMBL; AY016009; AAG39022.1; -.
 DR EMBL; BC017779; AAH17779.1; -.
 DR Genew; HGNC;14466; JAM2.
 DR MIM; 606870; -.
 DR GO; GO:0005887; C:integral to plasma membrane; NAS.
 DR GO; GO:0016337; P:cell-cell adhesion; NAS.
 DR InterPro; IPR007110; Ig_C2.
 DR InterPro; IPR003598; Ig_MHC.
 DR SMART; SM00408; IgC2_1; 2.
 DR PROSITE; PS50835; Ig_LIKE; 2.
 KW Immunoglobulin domain; Glycoprotein; Transmembrane; Signal.
 FT SIGNAL 1 20
 PT CHAIN 21 298 JUNCTIONAL ADHESION MOLECULE 2.
 PT DOMAIN 21 238 EXTRACELLULAR (POTENTIAL).
 PT TRANSMEM 239 259 POTENTIAL.
 PT DOMAIN 260 298 CYTOPLASMIC (POTENTIAL).
 PT DOMAIN 32 127 IG-LIKE V-TYPE.
 PT DOMAIN 134 238 IG-LIKE C2-TYPE.
 PT DISULFID 50 109 POTENTIAL.
 PT DISULFID 155 214 N-LINKED (GLCNAC. . .) (POTENTIAL).
 PT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
 PT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).
 PT SEQUENCE 236 236 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 298 AA; CA788518E22DCAEE CRC64;

 Query Match 29.5%; Score 483; DB 1; Length 29;
 Best Local Similarity 36.2%; Pred. No. 1.6e-33; CC
 Matches 115; Conservative 59; Mismatches 116; Index 28; Gaps 10; CC

 Qy 1 MALRPPRLRCLRPDFLLFRGCLIG----AVNLKSSNRTPVVQ--EFESVELSC 53
 Db 1 MARRSHRL-----LLLLRLIVVALGYHKAYGFSAPKDQQVTTAVEYQEALAC 50

 Qy 54 ITDSQTSDPTEWKIQLQDEQTYVFFDNKIQGLDAEFLGKTSUKIWNTRRSALY 113
 Db 51 -KTPKKTVSSRLWKKL-GRSVSFVVYQTLQGDFKRNREMI-DFNTRKVNTRSDAGKY 107

 Qy 114 RCEVVARNDR-KBIDEIVIELTVQVKPTVCRVPKAAPVGKMATHCQBSGHPRHYS 172
 Db 108 RCEVSAPESEQQNLEETVTLEVAPAVPSCEVPSAALSCTVVERLCQDEGNPAPEYT 167

 Qy 173 WYRNDVPLTDTSRANPRFRNSHHLNSEGTGLVFTAVHDGSQYYCIAANDGASARCEE 232
 Db 168 WFKDGIRLLENPLGSOSTNTSSYMTNTKGTLQFNTVSKLDGEYSEARNSGVTRCPG 227

 Qy 233 QMEEVYDNLINIGGIGVYVVALYLITLGICCAYRGYFINKQDGESYKNPGKEDGVN 292
 Db 228 KRMQVDDINISGIIAAVWVVALVISVGGLGVCYAQRKGYF-SKE--TSFQ--KSNSS 280

Qy 293 YIRTDEEGDRHKSSSFVI 310
 Db 281 KATINSENDPHTKFII 298

 RESULT 2
 JAM1_MOUSE STANDARD: PRT; 300 AA.
 AC 088792;
 DR 16-OCT-2001 (Rel. 40, Created)
 DR 16-OCT-2001 (Rel. 40, Last annotation update)
 DR 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Junctional adhesion molecule 1 precursor (JAM).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Butiharia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1] _TAXID=10090;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=983277120; PubMed=9660867;
 RA Martin-Padura I.; Lostaglio S.; Schneemann M.; Williams L.; Romano M.;
 RA Fruscella P.; Panzeri C.; Stoppacciaro A.; Ruco L.; Villa A.;
 RA Simmons D.; Delana E.;
 RT "Junctional adhesion molecule, a novel member of the immunoglobulin
 superfamily that distributes at intercellular junctions and modulates
 RT monocyte transmigration";
 RL J. Cell Biol. 142:117-127(1998).
 [2]
 RN [12]
 RP INTERACTION WITH PARD3.
 RX PubMed=11447115;
 RA Ebnat K.; Suzuki A.; Horikoshi Y.; Hirose T.;
 RA Meyer zu Brichwede M.-K.; Ohno S.; Vestweber D.;
 RT "The cell polarity protein ASIP/PAR-3 directly associates with
 junctional adhesion molecule (JAM)." ;
 RL EMBO J. 20:3738-3748(2001).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 212-238.
 RX PubMed=11500366;
 RA Kostrewa D.; Brockhaus M.; D'Arcy A.; Dale G.E.; Nelboeck P.;
 RA Schmid G.; Mueller F.; Bazzoni G.; Dejana E.; Bartfai T.;
 RA Winkler F.K.; Hennig M.;
 RT "X-ray structure of junctional adhesion molecule: structural basis for
 homophilic adhesion via a novel dimerization motif." ;
 RL EMBO J. 20:4391-4398(2001).
 CC -!- FUNCTION: Seems to plays a role in epithelial tight junction
 CC formation. Appears early in primordial forms of cell junctions and
 CC recruits PARD3. The association of the PARD6-PARD3 complex may
 CC prevent the interaction of PARD3 with JAM1, thereby preventing
 CC tight junction assembly. Plays a role in regulating monocyte
 CC transmigration involved in integrity of epithelial barrier.
 CC Involved in platelet activation.
 CC -!- SUBUNIT: Interacts with the first PDZ domain of PARD3. The
 CC association between PARD3 and PARD6 probably disrupts this
 CC interaction.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential)
 CC Localized at tight junctions of both epithelial and endothelial
 CC cells.
 CC -!- TISSUE SPECIFICITY: Localized at tight junctions of both
 CC epithelial and endothelial cells.
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
 CC -----
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 EMBL; U89915; AAC32382.1; -.
 DR 1F97; 22-AUG-01.
 DDBJ; 1F97; 22-AUG-01.

DR MGI:1321398; F1lr.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_v.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_v.
 DR SMART; SM00406; Ig_LIKE; 1.
 DR PROSITE; PS50835; Ig_LIKE; 2.
 DR Tight Junction; Immunoglobulin domain; Glycoprotein; Transmembrane;
 KW Tight junction; Immunostructure.
 KW Signal; 3D-structure.
 FT SIGNAL 1 26 POTENTIAL.
 FT CHAIN 27 300 JUNCTIONAL ADHESION MOLECULE 1.
 FT DOMAIN 27 238 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 239 259 POTENTIAL.
 FT DOMAIN 260 299 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 28 122 IG-LIKE V-TYPE 1.
 FT DOMAIN 134 230 IG-LIKE V-TYPE 2.
 FT DISULFID 49 108 POTENTIAL.
 FT DISULFID 152 212 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 42 42 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 300 AA; 32368 MW; 391F3E48FF3B97BC CRC64;

Query Match 27.5%; Score 449.5; DB 1; Length 300;
 Best Local Similarity 35.2%; Pred. No. 1.1e-30;
 Matches 105; Conservative 56; Mismatches 122; Indels 15; Gaps 7;

Qy 20 LLLLFRQCLIGAV----NLKSNRNPVQKFESVELSCLITDSQTSDFPRIEWKIKIQDEQ 74
 Db 11 LLLFLFTSMILGSLVQKGGSVTAQSDVQPVENESIKLT--TYSGFSSSPRYEWKEVQGST 68
 Qy 75 TTYYFFDNKIQDGLAAREILGKTSKLKIMWNTRDSALYRCVEVARNDRKEIDEVIELT 134
 Db 69 TALVCYNSQITAPYADRV-TFSSSGITFSSVTRKONGEYTC-MVSBEGGQNYGEISHLT 126
 CC -1- TISSUE SPECIFICITY: Localized at tight junctions of both
 epithelial and endothelial cells.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.

Qy 135 VQVKPVTCPVRCPKAVPGKMATLCOSEGHPRPHYSWTRNDVPLPT-DSRANPRFRNS 193
 Db 127 VLVPSPSKPTISPVSSSTVGNRAVLTSEHDGSPPSYE/SWFQDGISMLTDAKKTRAFMNS 186

Qy 194 SSHLNSETGTLYTAVKRDDQQYCLASNDAGSA-RCEEGQMEYVDLNIGCGIIGGVVV 252
 Db 187 SFTIDPKSGDLIFDPVTAFDSSGEYVQAOQNGYTAMRSAAHMDAVELNVGIVAAVLT 246

Qy 253 LAVLAATLGICCAYRGYFINKKODGESEYKNGPKGDGVNVTDTBEDGDFRKSSFPVI 310
 Db 247 LILGLLFLFGWFEASGYFETTKKG---TAPGKRVVYQSPTRGEFQTSSLV 300

RESULT 3
 JAM1_HUMAN STANDARD; PRT; 299 AA.
 AC Q9Y624;
 AC 16-OCT-2001 (Rel. 40, Created)
 AC 16-OCT-2001 (Rel. 40, Last sequence update)
 AC 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Junctional adhesion molecule 1 precursor (JAM molecule 1) (PAM-1) (Platelet F11 receptor).
 GN F11R OR JAM1 OR JCAM.
 OS Homo sapiens (Human).
 OC Mammalia; Chordata; Craniata; Vertebrata; Butelostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TAXID=9606;
 RN [1] SEQUENCE FROM N.A.
 RN MEDLINE=99123940; PubMed=10395639;
 RA Ozaki H., Ishii K., Horiuchi H., Arai H., Kawamoto T., Okawa K., Iwamatsu A., Kita T.,
 RT "Combined treatment of TNF-alpha and IFN-gamma causes redistribution of junctional adhesion molecule molecule in human endothelial cells.";
 RL J. Immunol. 163:553-557(1999).

RN [2] SEQUENCE FROM N.A.
 RA Sobocki T., Rushbrook J.I., Banerjee P., Weiss C., Kornecki E.;

Query Match	25.6%;	Score 419;	DB 1;	Length 299;	
Best Local Similarity	32.8%;	Pred. No.	4e-28;		
Matches 101;	Conservative	47;	Mismatches	138;	Indels 22;
					Gaps 7;
Y 8	RRLCARLPPFFLLFRGCLIGAVNLKSNRTPVYQEEFSEVELSCTITSDPRIEW 67				
Y 9	RKLCLC---FILALIUCSALGSVTSPEVRIPENNPKLSCAY--SGFSSPRAEW 62				
Y 68	KKIQEQTYYFEDNKIQDLAGRAELIGTSLSKIMNVTRDSALYRCEVYARNDRKEID 127				
Y 63	KFDQGDTRLVCNNKTTASYEDRTVFL-PGTTFSVTRDTGTYC-MVSEEGGNSYG 120				
Y 128	EIVIETVQRPTPVCRPKAVPVGORMATURQCBESGHAPPHYSWRNDVPLPTDSRAN 187				
Y 121	EVKVLIVLWPLPSKPTVNIPASSATIGNRAVLTCTSEQDGSPPSEYTWFKGIVMPNPKST 180				
Y 188	PRFRNSSLHNLSETGTLVFTAVHKDQGQYCYTASNDAGASARCEEQ-EIMEYVDLNIGGI 246				
Y 181	RAFSNYYVNVNPPTGHLFPLASDGTGEYCEARNYGTPTNTSNAVRMEAVERNVGIVV 240				
Y 247	GGLVVLAVALITLGICCAVGRGYFINNKQDGES---YKNPGKPDGVVNYIRTDEGGDF 302				
Y 241	AAVLYTLILIGLVLFPIWPAFSGHDTRKGTSSKKVIVYIOPS-----ARSEGF 291				
Y 303	RHKSSSFVI 310				
Y 292	KQTSSFLV 299				
RESULT 4					
AM1_BOVIN	JAMI_BOVIN	STANDARD;	PRT;	298 AA.	
Q9X756;					
16-OCT-2001	(Rel. 40, Created)				
16-OCT-2001	(Rel. 40, Last sequence update)				
15-SEP-2003	(Rel. 42, Last annotation update)				
Junctional adhesion molecule 1 precursor (JAM1)					
F11R OR JAM1					
Bos taurus (Bovine)					
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;					
Bovidae; Bovinae; Bos.					
NCBI_TaxID=9913;					
[1]					
SEQUENCE FROM N.A.					
SEQUENCE FROM N.A.					
MEDLINE=92323940;	PubMed=10395639;				
Ozaki H., Ishii K., Horiuchi H., Arai H., Kawamoto T., Okawa K.,					
Iwamatsu A., Kita T.,					
"Combined treatment of TNF-alpha and IFN-gamma causes redistribution of junctional adhesion molecule in human endothelial cells."					
J. Immunol. 163:553-557 (1999).					
-!- FUNCTION: Seems to play a role in epithelial tight junction formation. Appears early in primordial forms of cell junctions and recruits PARD3. The association of the PDZ6-PARD3 complex may prevent the interaction of PARD3 with JAM1, thereby preventing tight junction assembly (By similarity). Plays a role in regulating monocyte transmigration involved in integrity of epithelial barrier. Involved in platelet activation.					
-!- SUBUNIT: Interacts with the first PDZ domain of PARD3. The association between PARD3 and PARD6 probably disrupts this interaction (By similarity).					
-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).					
-!- TISSUE SPECIFICITY: Localized at tight junctions of both epithelial and endothelial cells.					
-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.					
-!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.					
RESULT 5					
A33_HUMAN	STANDARD;	PRT;	319 AA.		
ID					
AC	Q9795;				
DT	01-NOV-1997	(Rel. 35, Created)			
DT	01-NOV-1997	(Rel. 35, Last sequence update)			
DT	15-SEP-2003	(Rel. 42, Last annotation update)			
DE					
GN	GPA33.				
OS	Homo sapiens (Human)				
OC	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Catarrhini; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.				
RC	RC				
TISSUE=Colon carcinoma;					
MEDLINE=7165045;	PubMed=90280;				
RA	Health J.K., White S.J., Johnstone C.N., Catimel B., Simpson R.J.,				
RA	Moritz R.L., Tu G.-F., Ji H., Whitehead R.H., Green L.C.,				
RA	Scott M., Ritter G., Cohen L., Welt S., Old L.J., Nice E.C.,				
RA	Burgess A.W.				

DR	Pfam; PF00041; fn3; 2.	RN	SEQUENCE FROM N.A.
DR	Pfam; PF00047; 19; 5.	RP	SEQUENCE FROM N.A.
DR	SMART; SM00060; FN3; 2.	RC	STRAIN=Oregon R;
DR	SMART; SM00408; IGC2; 5.	RC	MEDLINE=9902870; PubMed=3141062;
DR	PROSITE; PS00835; IG_LIKE; 5.	RX	RX
KW	Cell adhesion; Glycoprotein; Transmembrane; Repeat; Brain;	RA	Seger M.A.; Haffley L.; Kaufman T.C.;
KW	Immunoglobulin domain; Alternative splicing; Signal.	RT	"Characterization of amalgam: a member of the immunoglobulin superfamily from <i>Drosophila</i> .";
FT	SIGNAL 1 19	RT	superfamily from <i>Drosophila</i> .";
CHAIN	20 1088	RL	Cel1 55:589-600(1988).
PT	NEURAL CELL ADHESION MOLECULE 1, 180 kDa	RN	[1]
PT	ISOFORM.	RN	SEQUENCE FROM N.A.
PT	EXTRACELLULAR (POTENTIAL).	RP	SEQUENCE FROM N.A.
PT	POTENTIAL.	RC	STRAIN=Berkeley;
PT	TRANSMEM	RC	Celniker S.E.; Pfeiffer B.D.; Knafeis J.; Martin C.H.; Mayeda C.A.;
PT	DOMAIN	RA	Medline=20196006; PubMed=10731132;
PT	706 723	RA	Celniker S.E.; Scherer S.E.; Li P.W.; Hostins R.A.; Galle R.F.;
PT	DOMAIN	RA	Palazzolo M.J.;
PT	1088	RA	"Complete sequence of the Antennapedia complex of <i>Drosophila</i> .";
PT	DOMAIN	RA	Submitt (JAN-1999) to the EMBL/GenBank/DBJ databases.
PT	20 108	RN	[2]
PT	HEPARIN-BINDING (POTENTIAL).	RN	SEQUENCE FROM N.A.
PT	FIBRONECTIN TYPE-III 1.	RP	SEQUENCE FROM N.A.
PT	FIBRONECTIN TYPE-III 2.	RC	STRAIN=Berkeley;
PT	HEPARIN-BINDING (POTENTIAL).	RC	Medline=20196006; PubMed=10731132;
PT	IG-LIKE C2-TYPE 3.	RA	George R.A.; Lewis S.E.; Richards C.E.; Holt R.A.; Evans C.A.; Gocayne J.D.;
PT	IG-LIKE C2-TYPE 4.	RA	Adams M.D.; Celminier S.E.; Yandell M.D.; Zhang Q.; Chen L.X.;
PT	IG-LIKE C2-TYPE 5.	RA	Sutton G.G.; Wortman J.R.; Pfeiffer B.D.;
PT	IG-LIKE C2-TYPE 1.	RA	Brandon R.C.; Rogers Y.H.C.; Blazej R.G.; Champe M.;
PT	IG-LIKE C2-TYPE 2.	RA	Wan K.H.; Doyle C.; Baxter E.G.; Helt G.; Nelson C.R.; Miklos G.L.G.;
PT	IG-LIKE C2-TYPE 3.	RA	Abril J.F.; Aghayani A.; An H.-J.; Andrews Pfanmoch C.; Baldwin D.;
PT	IG-LIKE C2-TYPE 4.	RA	Ballew R.M.; Basu A.; Baxendale J.; Bayraktaroglu L.; Beasley E.M.;
PT	IG-LIKE C2-TYPE 5.	RA	Beeson K.Y.; Benos P.V.; Berman B.P.; Bhandari P.; Boleshakov S.;
PT	DISULFID 41 93	RA	Borkova D.; Botchan M.R.; Bouck J.; Brodtier P.; Brottier P.;
PT	DISULFID 136 186	RA	Burts K.C.; Busam D.A.; Butler H.; Cadieu E.; Center A.; Chandra I.;
PT	DISULFID 232 282	RA	Cherry J.M.; Cawley S.; Dahlke C.; Davenport L.B.; Davies P.;
PT	DISULFID 323 379	RA	de Pablo B.; Delcher A.; Deng Z.; Dietz S.M.;
PT	DISULFID 420 473	RA	Dodson K.; Douc L.E.; Downes M.; Dugan-Rocha S.; Dunkov B.C.; Dunn P.;
PT	CARBOHYD 82 82	RA	Durbin K.J.; Evangelista C.C.; Ferraz C.; Ferriera S.; Fleischmann W.;
PT	CARBOHYD 219 219	RA	Foster C.; Gabriel A.E.; Garg N.S.; Gelbart W.M.; Glasser K.;
PT	CARBOHYD 310 310	RA	Gloede A.; Gong F.; Gorrell J.H.; Gu Z.; Guan P.; Harris M.;
PT	CARBOHYD 341 341	RA	Harris N.L.; Harvey D.; Heiman T.J.R.; Hernandez J.R.; Hrouck J.;
PT	CARBOHYD 417 417	RA	Hostin D.; Houston K.A.; Howland T.J.; Wei M.-H.; Ikegami C.;
PT	CARBOHYD 443 443	RA	Jalali M.; Kalush F.; Karpen G.H.; Ke Z.; Kennison J.A.; Ketchum K.A.;
PT	CARBOHYD 472 472	RA	Kimmel B.E.; Kodira C.D.; Kraft C.; Kravitz S.; Kulp D.; Lai Z.;
PT	VARSPLIC 804 1049	RA	Lasko P.; Lei Y.; Levitsky A.A.; Li J.; Li Z.; Liang Y.; Lin X.;
PT	Missing (in isoform N-CAM 14).	RA	Liu X.; Mattei B.; McIntosh T.C.; McLeod M.P.; McPherson D.;
PT	Missing (in isoform N-CAM 14).	RA	Merkulov G.; Milshina N.V.; Nobary C.; Morris J.; Mosherfi A.;
PT	Missing (in isoform N-CAM 14).	RA	Mount S.M.; Moy M.; Murphy B.; Murphy L.; Murry D.M.; Nelson D.R.;
PT	Missing (in isoform N-CAM 14).	RA	Nelson D.R.; Nelson K.A.; Nixon K.; Nusskern D.R.; Pacleb J.M.;
PT	Missing (in isoform N-CAM 14).	RA	Palazzolo M.; Pittman G.S.; Pan S.; Pollard J.; Scheeler F.; Shen H.;
PT	Missing (in isoform N-CAM 14).	RA	Reinert K.; Remington K.; Saunders R.D.C.; Shiebler F.; Shiebler F.; Shiebler F.;
PT	Missing (in isoform N-CAM 14).	RA	Shiebler F.; Shiebler F.; Shiebler F.; Shiebler F.;
PT	Missing (in isoform N-CAM 14).	RA	Shiebler F.; Shiebler F.; Shiebler F.; Shiebler F.;
PT	Missing (in isoform N-CAM 14).	RA	Shiebler F.; Shiebler F.; Shiebler F.; Shiebler F.;
PT	Missing (in isoform N-CAM 14).	RA	Spier E.; Spradling A.C.; Stapleton M.; Strong R.; Sun E.;
PT	Missing (in isoform N-CAM 14).	RA	Svirskas R.; Tector C.; Turner R.; Venter R.; Wang A.H.; Wang X.;
PT	Missing (in isoform N-CAM 14).	RA	Wang Z.-Y.; Wassarman D.A.; Weinstein G.M.; Weissenbach J.J.;
PT	Missing (in isoform N-CAM 14).	RA	Williams S.M.; Woodage T.; Worley K.C.; Wu D.; Yang S.; Yao Q.A.;
PT	Missing (in isoform N-CAM 14).	RA	Ye J.; Yeh R.-F.; Zaveri J.S.; Zhan M.; Zhang G.; Zhao Q.; Zheng L.;
PT	Missing (in isoform N-CAM 14).	RA	Zheng X.H.; Zhong F.N.; Zhou X.; Zhu S.; Zhu X.; Smith H.O.;
PT	Missing (in isoform N-CAM 14).	RA	Gibbs R.A.; Myers E.W.; Rubin G.M.; Venter J.C.;
PT	"The genome sequence of <i>Drosophila melanogaster</i> ."	RA	RT
PT	Score 11.4#;	RL	Science 297:2185-2195(2000).
Qy	Best Local Similarity 29.9#;	RN	[4]
Qy	29 9#;	RN	SEQUENCE FROM N.A.
Qy	Pred. No. 9e-08;	RP	SEQUENCE=Berkeley; TISSUE=Embryo;
Qy	Matches 63; Conservative 30; Mismatches 82; Indels 36; Gaps 12;	RC	MEDLINE=2242606; PubMed=12537569;
Db	30 GAVNLK----SSNRTPVQEPESEVLSCLTDSQTSRPL-IEWK-KIODEQTYYFFDN 82	RA	ID AMAL_DROME STANDARD; AC P15364_Q9v3A5; DT 01-APR-1990 (Rel. 14, Created)
Db	105 GTVNLIKQYKLQFLFKNAQPQERGEGADVAVIRCDVSSPSITWRKGKD-----VIFRK 159	RA	DT 16-OCT-2001 (Rel. 40, Last sequence update)
Qy	83 KIQGDLLGRAEILGKTSLIKIVNTRRSALYRCE--VVARND--RKEIDEVY-IELTVQ 137	RA	DT 15-SEP-2003 (Rel. 42, Last annotation update)
Db	160 DV-----RFVVLANNVQIQRGKTKUTGTYCEGRGLARGINYKDQIVVNPPPTQA 213	RA	DE Amalgam protein precursor.
Qy	138 KPVTPVGRVPKAVPGVKATHLCQESEGHPRHYSWNRDVLPLPTSQRNFRNSSSH 197	RA	GN AMB:BG:DS00276.6 OR CG2198.
Db	2114 RQI----RVNATANMAESSVVLSC-DAAGFPDPBEISWLKGKEPI-EDGEKISF----- 260	RA	OS Drosophila melanogaster (fruit fly).
Qy	198 NSETGTLLVTFAYKDDSGQYCCIASNDAGSA 228	RA	OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Db	2611 NEDQSENTTHYKEKDDEAEYCKANNQAGEA 291	RA	OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Qy	"The genome sequence of <i>Drosophila melanogaster</i> ."	RA	OC Ephydioidea; Drosophilidae; Drosophila.
Db	RESULT 7	RA	NCBI TaxID=7227;
AMAL_DROME	STANDARD;	RA	CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
ID AMAL_DROME	P15364_Q9v3A5;	AC	CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
AC P15364_Q9v3A5;	PRT; 333 AA.	DT	CC --- This SWISS-PROT entry is copyright. It is produced through a collaboration
DT 01-APR-1990 (Rel. 14, Created)	RA	CC between the Swiss Institute of Bioinformatics and the EMBL outstation -	
DT 16-OCT-2001 (Rel. 40, Last sequence update)	RA	CC ---	
DT 15-SEP-2003 (Rel. 42, Last annotation update)	RA	CC ---	
DE Amalgam protein precursor.	RA	CC ---	
GN AMB:BG:DS00276.6 OR CG2198.	RA	CC ---	
OS Drosophila melanogaster (fruit fly).	RA	CC ---	
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;	RA	CC ---	
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	RA	CC ---	
OC Ephydioidea; Drosophilidae; Drosophila.	RA	CC ---	
NCBI TaxID=7227;	OX	CC ---	

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CC	EMBL; M23561; AAB28367.1; -;	RX MEDLINE=93273329; PubMed=7684721;
CC	EMBL; AE001572; AAD1997.1; -;	RA Tonissen K.F.; Krieg P.A.;
CC	EMBL; AE003674; AAF54084.1; -;	RT "Two neural-cell adhesion molecule (NCAM)-encoding genes in Xenopus laevis are expressed during development and in adult tissues.";
CC	DR PIR; A31923; A311923.	RT Gene 127:243-247(1993).
CC	DR FLYBase; Fgn0000071; Ama.	-!- FUNCTION: THIS PROTEIN IS A CELL ADHESION MOLECULE INVOLVED IN NEURON-NEURON ADHESION, NEURITE FASCICULATION, OUTGROWTH OF NEURITES, ETC.
CC	GO; GO:0005886; C:Plasma membrane; IDA.	-!- SUBCELLULAR LOCATION: Type I membrane protein.
CC	DR InterPro; IPR007110; Ig-like.	-!- ALTERNATIVE PRODUCTS:
CC	DR InterPro; IPR003598; Ig-c2.	Comment=A number of isoforms are produced;
CC	DR SMART; SM00408; IgC2; 2.	Name=1;
CC	DR SMART; SM00835; Ig_LIKE; 3.	IsoId=P36335-1; Sequence=Displayed;
CC	DR Immunoglobulin domain; Glycoprotein; GPI-anchor; Signal; Repeat; SIGNAL 1 23 POTENTIAL.	-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
FT	FT CHAIN 24 ?	CC -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
FT	FT PROPEP 2 ?	CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
FT	FT DOMAIN 25 128	CC -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
FT	FT DOMAIN 139 223	CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
FT	FT DOMAIN 230 323	CC -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
FT	FT DISULFID 46 117	CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
FT	FT DISULFID 161 208	CC -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
FT	FT DISULFID 251 307	CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
FT	FT CARBOHYD 45 45	DR HSSP; P56276; ITLK.
FT	FT CARBOHYD 86 86	DR Intertiro; IPR003961; FN III.
FT	FT CARBOHYD 308 308	DR Intertiro; IPR007110; Ig-like.
FT	FT CONFLICT 83 83	DR Intertiro; IPR00398; Ig-C2.
SQ	SQ SEQUENCE 333 AA: 36387 MW: F644753DE3DB25FL CRC64;	DR Intertiro; IPR00306; Ig MHC.
Qy	Qy 35 KSSNRTPVQEFPSVLSCLITDSQTSPRTEWKQIODECTYYFFDNKIQGDLAGRAEI 94	DR PIR; JN0635; JN0635.
Db	Db 143 ENTPKSTIVTEGNLELTC--HANGFPKPTISWAR-----ERNAVMPAGHL 187	DR HSSP; P56276; ITLK.
Qy	Qy 95 LGKTSKLKWNTTRDSDALYRCEVVARNDKKEDEVITLVQVKPVTVPVCRPKAVPGK 154	DR Intertiro; IPR003961; FN III.
Db	Db 188 LAEPTLRTSRVHMDRGCGYYC--IAQNGEGQPDFKRLIRVEFEPRQTAQREPKLAQMVSII 245	DR Intertiro; IPR007110; Ig-like.
Qy	Qy 155 MATLHQSESEGHRPHYSWYRDVPLPTDSRANPRFNSSSSHLNSETGTVTAVERKDD 214	DR Intertiro; IPR00398; Ig-like.
Db	Db 246 SAELEC-SVQGYPAPTVWHKNGVPL--QSSRHEVANTASSGGTTSVLRIDSVEEDF 302	DR Intertiro; IPR00306; Ig MHC.
Qy	Qy 215 GOYCIASNDAGSA 228	DR SMART; SM00408; Ig_LIKE; 4.
Db	Db 303 GDYCNATNKUJGHA 316	DR PROSITE; PS50835; Ig_LIKE; 5.
Matches	Matches 52; Conservative 39; Mismatches 83; Indels 20; Gaps 5;	KW Cell adhesion; Glycoprotein; Transmembrane; Repeat; Brain;
Qy	Qy 35 KSSNRTPVQEFPSVLSCLITDSQTSPRTEWKQIODECTYYFFDNKIQGDLAGRAEI 94	KW Immunoglobulin domain; Alternative splicing; Signal.
Db	Db 143 ENTPKSTIVTEGNLELTC--HANGFPKPTISWAR-----ERNAVMPAGHL 187	FT SIGNAL 1 19 BY SIMILARITY.
Qy	Qy 35 KSSNRTPVQEFPSVLSCLITDSQTSPRTEWKQIODECTYYFFDNKIQGDLAGRAEI 94	FT CHAIN 20 1092 NEURAL CELL ADHESION MOLECULE 2, 180 kDa ISOFORM.
Qy	Qy 95 LGKTSKLKWNTTRDSDALYRCEVVARNDKKEDEVITLVQVKPVTVPVCRPKAVPGK 154	FT DOMAIN 20 705 EXTRACELLULAR (POTENTIAL).
Db	Db 188 LAEPTLRTSRVHMDRGCGYYC--IAQNGEGQPDFKRLIRVEFEPRQTAQREPKLAQMVSII 245	FT DOMAIN 706 723 POTENTIAL.
Qy	Qy 155 MATLHQSESEGHRPHYSWYRDVPLPTDSRANPRFNSSSSHLNSETGTVTAVERKDD 214	FT DOMAIN 724 1092 CYTOSMERIC (POTENTIAL).
Db	Db 246 SAELEC-SVQGYPAPTVWHKNGVPL--QSSRHEVANTASSGGTTSVLRIDSVEEDF 302	FT DOMAIN 20 108 IG-LIKE C2-TYPE 1.
Qy	Qy 215 GOYCIASNDAGSA 228	FT DOMAIN 113 202 IG-LIKE C2-TYPE 2.
Db	Db 303 GDYCNATNKUJGHA 316	FT DOMAIN 208 295 IG-LIKE C2-TYPE 3.
Qy	Qy 35 KSSNRTPVQEFPSVLSCLITDSQTSPRTEWKQIODECTYYFFDNKIQGDLAGRAEI 94	FT DOMAIN 303 397 IG-LIKE C2-TYPE 4.
Db	Db 143 ENTPKSTIVTEGNLELTC--HANGFPKPTISWAR-----ERNAVMPAGHL 187	FT DOMAIN 400 489 IG-LIKE C2-TYPE 5.
Qy	Qy 95 LGKTSKLKWNTTRDSDALYRCEVVARNDKKEDEVITLVQVKPVTVPVCRPKAVPGK 154	FT DOMAIN 512 589 FIBRONECTIN TYPE-III 1.
Db	Db 188 LAEPTLRTSRVHMDRGCGYYC--IAQNGEGQPDFKRLIRVEFEPRQTAQREPKLAQMVSII 245	FT DOMAIN 618 686 FIBRONECTIN TYPE-III 2.
Qy	Qy 155 MATLHQSESEGHRPHYSWYRDVPLPTDSRANPRFNSSSSHLNSETGTVTAVERKDD 214	FT DOMAIN 149 153 HEPARING-BINDING (POTENTIAL).
Db	Db 246 SAELEC-SVQGYPAPTVWHKNGVPL--QSSRHEVANTASSGGTTSVLRIDSVEEDF 302	FT DOMAIN 158 162 HEPARING-BINDING (POTENTIAL).
Qy	Qy 215 GOYCIASNDAGSA 228	FT DISULFID 41 93 PROBABLE.
Db	Db 303 GDYCNATNKUJGHA 316	FT DISULFID 136 186 PROBABLE.
RESULT 8	NCA2_XENLA STANDARD; PRT; 1092 AA.	FT DISULFID 232 282 PROBABLE.
ID	ID NCNA2_XENLA STANDARD; PRT; 1092 AA.	FT DISULFID 323 379 PROBABLE.
AC	AC P36335;	FT DISULFID 420 473 PROBABLE.
DT	DT 01-JUN-1994 (Rel. 29, Created)	FT CARBOHYD 82 82 N-LINKED (GLCNAC. . .) (POTENTIAL).
DT	DT 01-JUN-1994 (Rel. 29, Last sequence update)	FT CARBOHYD 219 219 N-LINKED (GLCNAC. . .) (POTENTIAL).
DT	DT 15-SEP-2003 (Rel. 42, Last annotation update)	FT CARBOHYD 310 310 N-LINKED (GLCNAC. . .) (POTENTIAL).
DB	DB Neural cell adhesion molecule 2, 180 kDa isoform precursor (N-CAM 180).	FT CARBOHYD 341 341 N-LINKED (GLCNAC. . .) (POTENTIAL).
GN	GN NCAM2.	FT CARBOHYD 417 417 N-LINKED (GLCNAC. . .) (POTENTIAL).
OS	OS Xenopus laevis (African clawed frog).	FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).
OC	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;	FT CARBOHYD 472 472 N-LINKED (GLCNAC. . .) (POTENTIAL).
OC	OC Xenopoda; Xenopus.	SQ SEQUENCE 1092 AA; 118082 MW; CD236EE0FB7AD1 CRC64;
OX	OX NCBI_TAXID=8355;	Query Match 10 8%; Score 177; DB 1; Length 1092;
RN	RN [1]	Best Local Similarity 29 5%; Pred. No. 5.2e-07;
RP	RP Matches 62; Conservative 28; Mismatches 86; Indels 34; Gaps 11;	Matches 62; Conservative 28; Mismatches 86; Indels 34; Gaps 11;

Qy 30 GAVNLKSSNR----TPVQPFESVELSCITDSQTSDPR-IEWK-KIODEQQTTYVFEDN 82
 Db 105 GTVNLLKYYQKLTFKYA|PQPQFEGDAV|CDS|PSITW|HKGKD|---VIKK 159
 Qy 83 KIQGDLAGRAETLKGTSKLNVRDSDALYRCB--VVARNDRKELDEIVIETVQVKPV 140
 Db 160 DV-----RFVFLANNYLQIRGKIKTDEGNYRCGRILARG--EINYKDIQVITNVPPL 210
 Qy 141 TPV-CRVPKAVPVGKMATHCQESEFGHPRHYSWNRDYLPTDSRANPFRFRNNSHHN 198
 Db 211 IQARQRVNRATANMDESVLSTS-DADGFDPBISWLKGEDI-EDGEEKTSF-----N 261
 Qy 199 SETGTLYFTAVHKDDSGQCYCTASNDAGSA 228
 Db 262 EDKSEMTIYRVEKEDAEYSCSTANNAGEA 291

RESULT 9
 NCAM2_MOUSE ID _MOUSE STANDARD; PRT; 725 AA.
 AC P13564; O61950;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Neural cell adhesion molecule 1, 120 kDa isoform precursor (N-CAM 120)
 DB NCBI_TaxID:10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE=87246524; PubMed=1595563;
 RA Bartels D., Santoni M.-J., Wille W., Ruppert C., Caix J.-C.,
 RA Hirsch M.-R., Pontecilla-Camps J.-C., Goridis C.;
 RT "Isolation and nucleotide sequence of mouse NCAM cDNA that codes for
 RT a Mr 79,000 polypeptide without a membrane-spanning region.";
 RL EMBO J. 6:907-914 (1987).
 RN [2]
 RP SEQUENCE OF 20-700 FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=89215156; PubMed=212486;
 RA Santoni M.J., Barthels D., Vooper G., Boned A., Goridis C., Wille M.;
 RT "Differential exon usage involving an unusual splicing mechanism
 RT generates at least eight types of NCAM cDNA in mouse brain.";
 RL EMBO J. 8:385-392 (1989).
 RN [3]
 RP SEQUENCE OF 642-725 FROM N.A.
 RX MEDLINE=88283628; PubMed=3396534;
 RA Barbas J.A., Chaix J.C., Steinmetz M., Goridis C.;
 RT "Structural and immunological characterization of the amino-terminal
 domain of mammalian neural cell adhesion molecules.";
 RL J. Biol. Chem. 261:3396-3401 (1986).
 RT "FUNCTION: THIS PROTEIN IS A CELL ADHESION MOLECULE INVOLVED IN
 CC NEURON-NEURON ADHESION, NEURITE FASCICULATION, OUTGROWTH OF
 CC SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=N-CAM 120;
 CC IsoId=P13594-1; Sequence=Displayed;
 CC IsoId=P13595-1; Sequence=External;
 CC Name=N-CAM 140;

Qy 300 GAVNLKSSNR----TPVQPFESVELSCITDSQTSDPR-IEWK-KIODEQQTTYVFEDN 82
 Db 105 GTVNLLKYYQKLTFKYA|PQPQFEGDAV|CDS|PSITW|HKGKD|---VIKK 159
 Qy 83 KIQGDLAGRAETLKGTSKLNVRDSDALYRCB--VVARNDRKELDEIVIETVQVKPV 140
 Db 160 DV-----RFVFLANNYLQIRGKIKTDEGNYRCGRILARG--EINYKDIQVITNVPPL 210
 Qy 141 TPV-CRVPKAVPVGKMATHCQESEFGHPRHYSWNRDYLPTDSRANPFRFRNNSHHN 198
 Db 211 IQARQRVNRATANMDESVLSTS-DADGFDPBISWLKGEDI-EDGEEKTSF-----N 261
 Qy 199 SETGTLYFTAVHKDDSGQCYCTASNDAGSA 228
 Db 262 EDKSEMTIYRVEKEDAEYSCSTANNAGEA 291

CC IsoId=P13595-2; Sequence=External;
 CC -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
 CC -!- SIMILARITY: Contains 2 fibronectin type III domains.

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 CC or send an email to license@isb-sib.ch.

CC DR Y00051; CAA68263.1; -.
 DR EMBL; X15049; CAA31148.1; ALT_SEQ.
 DR EMBL; X02795; CAA30173.1; -.
 DR PIR; A29673; IJMSNG.
 DR PDB; 2NCM; 12-MAR-97.
 DR MGDB; MG1:9728; Ncami.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_C2.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00041; fn3; 2.
 DR Pfam; PF00047; 19; 5.
 DR SMART; SM00060; FN3; 2.
 DR PROSITE; PS50815; Ig_LikeB; 5.
 KW Cell adhesion; Glycoprotein; Repeat; Alternative splicing;
 KW Immunoglobulin domain; Signal; Heparin-binding; GPI-anchor;
 KW 3D-structure.

CC FT SIGNAL; 19
 CC FT CHAIN; 20
 CC FT DOMAIN; 20
 CC FT DOMAIN; 116
 CC FT DOMAIN; 212
 CC FT DOMAIN; 302
 CC FT DOMAIN; 309
 CC FT DOMAIN; 402
 CC FT DOMAIN; 407
 CC FT DOMAIN; 519
 CC FT DOMAIN; 625
 CC FT DOMAIN; 152
 CC FT DOMAIN; 161
 CC FT DISULFID; 41
 CC FT DISULFID; 139
 CC FT DISULFID; 235
 CC FT DISULFID; 330
 CC FT DISULFID; 427
 CC FT CARBOHYD; 222
 CC FT CARBOHYD; 316
 CC FT CARBOHYD; 348
 CC FT CARBOHYD; 424
 CC FT CARBOHYD; 450
 CC FT CARBOHYD; 479
 CC FT CARBOHYD; 600
 CC FT CONFLICT; 261
 CC FT CONFLICT; 273
 CC FT CONFLICT; 355
 CC FT CONFLICT; 549
 CC FT CONFLICT; 572
 CC FT CONFLICT; 575
 CC FT CONFLICT; 589
 CC FT CONFLICT; 600
 CC FT CONFLICT; 657
 CC FT CONFLICT; 725 AA; 80296 MW; C2AE8BA461C6B2F CRC64;

Query Match 10 5%; Score 171.5; DB 1; Length 725;
 Best Local Similarity 27.13%; Pred. No. 9.1e-07;
 Matches 63; Conservative 41; Mismatches 84; Indels 43; Gaps 12;

Qy 27 CLIGA-----VNLKSSNR----TPVQPFESVELSCITDSQTSDPS-DPRIBKQKIQ 71
 Db 96 CvvTEDGTQSEATVNVKIFQKMMFKNAPTQEFEKEGEDAVICDVSSLPTIWK-- 152

Qy	72 DEQTIVVFFDNKIQGDLAGRAEILGKTSKLWNVTREDSDALYRE--VVANDRKEIDEI 129
Db	153 ----HKGRDYLKCDV--RTFVLSNNYLQIRGIKTDEGYTRCEGRILARG--EINFK 202
Qy	130 VIELTYQVKPVTPVCR--VPKAVPVGRMATHCOSEGHPRPHYSWYRNDDPLPTDSRAN 187
Db	203 DIQIVVNPPTVQAROSIVNATANLGSVTLV-C-DAQFPPEPTMSWRDGEPJENEE-D 260
Qy	188 PRFRNSSSHLNSETGLVFTAVHKDGGOYCTIASNDGASARCEQEEMEVY 238
Db	261 ERSSEVY---SDSSEVTIRNDKNDAEYVTCIAENKAG----EQPASIH 302
RESULT 10	
NCAL_MOUSE	
ID	NCA_MOUSE STANDARD; PRT; 1115 AA.
AC	P13395; Q61949;
DT	01-JUN-1990 (Rel. 13, Created)
DT	01-JUL-1993 (Rel. 26, Last annotation update)
DT	15-SEP-2003 (Rel. 42, Last annotation update)
DE	Neural cell adhesion molecule 1, 180 kDa isoform precursor (N-CAM 180) (NCAM-180).
DB	GN NCAM1 OR NCAM.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC	NCBI_TaxID:10900;
OX	
RN	SEQUENCE FROM N.A. (ISOFORM N-CAM 180).
RC	STRAIN=C57BL/6; PubMed=87246524; PubMedId=3595563;
RX	MEDLINE=87246524;
RA	Barthels D., Santoni M.J., Wille W., Ruppert C., Chaix J.C., Hirsch M.R., Pontecilla-Camps J.C., Goridis C.,
RA	"Isolation and nucleotide sequence of mouse NCAM cDNA that codes for a Mr 79,000 polypeptide without a membrane-spanning region.";
RT	EMBO J. 6:907-914 (1987).
RL	
RN	SEQUENCE OF 529-1115 FROM N.A. (ISOFORM N-CAM 140).
RC	STRAIN=C57BL/6; PubMed=8606768; PubMedId=3684567;
RX	MEDLINE=8606768;
RA	Santoni M., Barthels D., Barbas J.A., Hirsch M.-R., Steinmetz M., Goridis C., Wille W.,
RA	"Analysis of cDNA clones that code for the transmembrane forms of the mouse neural cell adhesion molecule (NCAM) and are generated by alternative RNA splicing.";
RT	EMBO J. 7:625-632 (1988).
RL	Nucleic Acids Res. 15:8621-8641 (1987).
RN	SEQUENCE OF 642-1115 FROM N.A. (ISOFORM N-CAM 180).
RC	STRAIN=C57BL/6; TISSUE=Brain;
RX	MEDLINE=85283658; PubMed=336534;
RA	Barthels J.A., Chaix J.C., Steinmetz M., Goridis C.,
RA	"Differential splicing and alternative polyadenylation generates distinct NCAM transcripts and proteins in the mouse.";
RT	EMBO J. 7:625-632 (1988).
RL	Nucleic Acids Res. 16:4217-4225 (1988).
RN	SEQUENCE OF 702-1115 FROM N.A. (ISOFORM N-CAM 140).
RP	STRAIN=C57BL/6; TISSUE=Brain;
RC	MEDLINE=85283653; PubMed=2721406;
RX	Santoni M.J., Barthels D., Vopper G., Boned A., Goridis C., Wille M..
RA	"Differential exon usage involving an unusual splicing mechanism generates least eight types of NCAM cDNA in mouse brain.";
RT	EMBO J. 8:385-392 (1989).
RN	SEQUENCE OF 20-36.
RP	MEDLINE=8514020; PubMedId=3512556;
RX	

RA Rougon G., Marshak D.R.; "Structural and immunological characterization of the amino-terminal domain of mammalian neural cell adhesion molecules.", J. Biol. Chem. 261:3396-3401(1986).
 RT -1. FUNCTION: THIS PROTEIN IS A CELL ADHESION MOLECULE INVOLVED IN NEURON-NEURON ADHESION, NEURITE FASCICULATION, OUTGROWTH OF NEURITES, ETC.
 RT -1. SUBCELLULAR LOCATION: Type I membrane protein.
 RL -1. ALTERNATIVE PRODUCTS:
 CC -1. Event=Alternative splicing; Named isoforms=3;
 CC Name=CN-CAM 180;
 CC IsoID=PI3395-1; Sequence=Displayed;
 CC Name=CN-CAM 140;
 CC IsoID=PI3395-2; Sequence=VSP_0025988;
 CC Name=CN-CAM 120;
 CC IsoID=PI3394-1; Sequence=External;
 CC -1. SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -1. SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
 CC -1. SIMILARITY: Contains 2 fibronectin type III domains.
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 CC
 DR EMBL; Y0051; -; NOT_ANNOTATED_CDS.
 DR EMBL; X0328; CAA28671.1; -.
 DR EMBL; X0195; CAA30173.1; -.
 DR EMBL; X0244; CAA30230.1; -.
 DR EMBL; X1051; CAA31150.1; -.
 DR EMBL; X15052; CAA31151.1; -.
 DR PIR; A29673; JUMSNL.
 DR MGD; MGI_97281; Ncam1.
 DR InterPro; IPR003961; FN1-III.
 DR InterPro; IPR007110; Ig-Like.
 DR InterPro; IPR003598; Ig_C2.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00041; fn3; 2.
 DR Pfam; PF00047; 19; 5.
 DR SMART; SN00060; FN3; 2.
 DR SMART; SN00408; IgCC; 5.
 DR PROSITE; PS50835; IG_LIKE; 5.
 KW Cell adhesion; Glycoprotein; Transmembrane; Repeat; Signal; Heparin-binding
 KW Immunoglobulin domain; Alternative splicing; Signal; Heparin-binding
 SIGNAL 1 19
 CHAIN 20 1115 NEURAL CELL ADHESION MOLECULE 1, 180 kD
 FT DOMAIN 20 711 ISOFORM
 FT DOMAIN 712 729 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 730 1115 POTENTIAL.
 FT DOMAIN 20 111 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 116 205 IG-LIKE C2-TYPE 1.
 FT DOMAIN 212 302 IG-LIKE C2-TYPE 2.
 FT DOMAIN 309 402 IG-LIKE C2-TYPE 3.
 FT DOMAIN 407 492 IG-LIKE C2-TYPE 4.
 FT DOMAIN 519 596 IG-LIKE C2-TYPE 5.
 FT DOMAIN 625 692 FIBRONECTIN TYPE-III 1.
 FT DOMAIN 152 156 FIBRONECTIN TYPE-III 2.
 FT DOMAIN 161 165 HEPARIN-BINDING (POTENTIAL).
 FT DISULFID 41 96 HEPARIN-BINDING (POTENTIAL).
 FT DISULFID 139 189 PROBABLE.
 FT DISULFID 285 288 PROBABLE.
 FT DISULFID 235 288 PROBABLE.
 FT DISULFID 330 386 PROBABLE.
 FT DISULFID 427 480 PROBABLE.
 FT CARBOHYD 222 222 N-LINKED (GLCNAC, .) (POTENTIAL).
 FT CARBOHYD 316 316 N-LINKED (GLCNAC, .) (POTENTIAL).
 FT CARBOHYD 348 348 N-LINKED (GLCNAC, .) (POTENTIAL).
 FT CARBOHYD 424 424 N-LINKED (GLCNAC, .) (POTENTIAL).
 FT CARBOHYD 450 450 N-LINKED (GLCNAC, .) (POTENTIAL).

PT	CARBOHYD	479	479	N-LINKED (GLCNAC, .) (POTENTIAL) ;	
PT	VARSPLIC	810	1076	Missing (in isoform N-CAM 140) .	
SQ	SEQUENCE	1115 AA;	119351 MW;	2C93D0474CPBCAF CRC64 ;	
	Query Match	10.5%;	Score 171.5;	DB 1;	
	Best Local Similarity	27.3%;	Pred. No. 1.6e-06;	Length 1115;	
	Matches	63;	Conservative	41;	
	Mismatches	84;	Indels	43;	
	Gaps	12;			
Qy	27 CLIGA-----YNLKSSNR----TPVYQFESVELSCLTSQS-DPRIMEKKIQ 71				
Db	96 CTVTAEDGTQSEATVNKVLFQKLIMFKNAPTFKEGEADAVICDVVSLSLPTIWK--- 152				
Qy	72 DEQTYYFPFDNKIQGDLGRAEILGKTSKLMNVTRDSALYRC--VVARNDRKEIDEI 129				
Db	153 ----HRGRDVLTKKDV--RFIVLSSNNYLQRGIKTDEGYTCERILLARG--EINFK 202				
Qy	130 VIELTYVOKVPVFCR--VPKAPEVGRMATHQESEGHPRPHYSWYRNNDPLPTDSRAN 187				
Db	203 DIQIVINVPPTVQARQSVNATANLGOSVTLVCG-DAQGPPEPTMSAKTGDGPENEE-D 260				
Qy	188 PRFRNNSSHLNSETGTLLVFTATHKDDSGGQYCIAIASDAGSARCEQEMEVY 238				
Db	261 ERSRSSV---SDSSEVTVIRNDKNDAEYVCTIAENRA-G---EQDASIH 302				
RESULT 11					
ID	NEO1_RAT	STANDARD;	PRT;	1377 AA.	
AC	P97603;				
DT	16-OCT-2001	(Rel. 40, Created)			
DT	16-OCT-2001	(Rel. 40, Last sequence update)			
DT	15-SEP-2003	(Rel. 42, Last annotation update)			
	Neogenin precursor (Fragment).				
GN	NEO1 OR NGN.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OX	NCBI Taxid:1011;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE_Brain;				
RX	MEDLINE=97015074; PubMed=8861902;				
RA	Kaino-Matsu K., Matsui M., Hirai L., Leonardo E.D., Chan S.S.-Y.,				
RA	Keiutto J.G., Tessier-Lavigne M.,				
RT	"Deleted in Colorectal Cancer (DCC) encodes a netrin receptor.";				
RL	Cell 87:175-185 (1996).				
CC	-!- FUNCTION: MAY BE INVOLVED AS A REGULATORY PROTEIN IN THE TRANSITION OF UNDIFFERENTIATED PROLIFERATING CELLS TO THEIR DIFFERENTIATED STATE. MAY ALSO FUNCTION AS A CELL ADHESION MOLECULE IN A BROAD EXPRESSION OF EMBRYONIC AND ADULT TISSUES.				
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.				
CC	-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. DCC SUBFAMILY.				
CC	-!- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.				
CC	-!- SIMILARITY: Contains 6 fibronectin type III domains.				
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CC	DR: HSSP; P56276; AA841100.1; -.				
CC	InterPro; IPR003961; FN_III.				
CC	InterPro; IPR003962; FN_III_subd.				
CC	InterPro; IPR007110; Ig-like.				
CC	InterPro; IPR003598; Ig_C2.				
CC	InterPro; IPR00306; Ig_MHC.				
CC	PFam; PF00041; fn3; 6.				
RESULT 12					
ID	NCA1_RAT	STANDARD;	PRT;	858 AA.	
AC	P13596;				
DT	01-JAN-1990 (Rel. 13, Created)				
DT	01-JAN-1990 (Rel. 13, Last sequence update)				
DT	15-SEP-2003 (Rel. 42, Last annotation update)				
DE	Neural cell adhesion molecule 1, 140 kDa isoform precursor (N-CAM 140).				
GN	NCAMI OR NCAM.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Buteraria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
NCBI_TaxID=1011;					

CC	- - SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.	FT	VARSPLITC	609	1137	/FTId=VSP_005149.
CC	- - SIMILARITY: Contains 8 fibronectin type III domains.	FT	MUTAGEN	1178	1178	Missing (In isoform 3).
CC	- - SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.	FT	SEQUENCE	1912 AA;	214759 MW;	/FTId=VSP_005150.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	Query Match	10.4%	Score 169.5;	DB 1:	R->A: 2.5-TOLD REDUCTION IN CLEAVAGE.
CC	CC	Best Local Similarity	28.6%;	Pred. No. 4.5e-06;		
CC	Matches	65;	Conservative	35;	Mismatches	76;
CC	CC	Gaps	13;			
CC	CC	Db	Qy	39 RTPVQPFESVBLSCITDSOTSDPR-IEW---KKIQDEQTIVFFDNKIQGDLAGRA 92	Db	39 RTPVQPFESVBLSCITDSOTSDPR-IEW---KKIQDEQTIVFFDNKIQGDLAGRA 92
CC	CC	Db	Qy	28 RTPVDOTGVSGVGASFTCQA-TGDRPKIVNKKGKVSQRFETIEFDD-----GSG 79	Db	28 RTPVDOTGVSGVGASFTCQA-TGDRPKIVNKKGKVSQRFETIEFDD-----GSG 79
CC	CC	Db	Qy	93 EILGKTSLSK1WNVRDSDALYRCEVARNDRKEIDDIVELTVQVTPVTCRVPAVP 152	Db	93 EILGKTSLSK1WNVRDSDALYRCEVARNDRKEIDDIVELTVQVTPVTCRVPAVP 152
CC	CC	Db	Db	80 SVLRQPLR---TPRDEAIEC-YASNNNGEI-SVSTRITVLRD----QIPPGFPT 127	Db	80 SVLRQPLR---TPRDEAIEC-YASNNNGEI-SVSTRITVLRD----QIPPGFPT 127
CC	CC	Db	Qy	153 GKM-----ATLHCQESECHPRPHYSWYRNDDPLPTDSRANPRFRNSSSHLNSE 200	Db	153 GKM-----ATLHCQESECHPRPHYSWYRNDDPLPTDSRANPRFRNSSSHLNSE 200
CC	CC	Db	Db	128 IDMGPQLKVYERTRATMLCAAS-GNDPDTWFLPVDT-SNNNGRK-----OURSE 181	Db	128 IDMGPQLKVYERTRATMLCAAS-GNDPDTWFLPVDT-SNNNGRK-----OURSE 181
CC	CC	Db	Qy	201 T-----GTLVFTAHVHKDDSGQYQYCLASNDGARCEQEMEVYDL 240	Db	201 T-----GTLVFTAHVHKDDSGQYQYCLASNDGARCEQEMEVYDL 240
CC	CC	Db	Db	182 SIGGTPIRGALQIEQSBSEDSGKYECAVTNSAGTYSAPANLYTEL 228	Db	182 SIGGTPIRGALQIEQSBSEDSGKYECAVTNSAGTYSAPANLYTEL 228
CC	CC	RESULT 14				
CC	CC	NCM2_HUMAN	STANDARD;	PRT;	837 AA.	
CC	CC	ID	NCM2_HUMAN			
CC	CC	AC	O15350;			
CC	CC	DT	15-JUL-1998 (Rel. 36, Created)			
CC	CC	DT	15-JUL-1998 (Rel. 36, Last sequence update)			
CC	CC	DR	15-SEP-2003 (Rel. 42, Last annotation update)			
CC	CC	DB	Neural cell adhesion molecule 2 precursor (N-CAM 2).			
CC	CC	GN	NCAM2 OR NCAM21.			
CC	CC	OS	Homo sapiens (Human).			
CC	CC	OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
CC	CC	OC	NCBI_TaxID=9606;			
CC	CC	OX	NCBI_TaxID=9606;			
CC	CC	RP	SEQUENCE FROM N.A.			
CC	CC	RC	SEQUENCE FROM N.A.			
CC	CC	RX	SEQUENCE FROM N.A.			
CC	CC	RA	"Cloning of a novel human neural cell adhesion molecule gene (NCAM2) that maps to chromosome region 21q21 and is potentially involved in Paoloni-Giacobino A., Chen H., Antonarakis S.E.;			
CC	CC	RA	RT Down syndrome"; PubMed=9226371;			
CC	CC	RA	RT MEDLINE=97139930; PubMed=9226371;			
CC	CC	RA	RT PAOLONI-GIACOBINO A., CHEN H., ANTONARAKIS S.E.;			
CC	CC	RA	RT "Cloning of a novel human neural cell adhesion molecule gene (NCAM2) that maps to chromosome region 21q21 and is potentially involved in Paoloni-Giacobino A., Chen H., Antonarakis S.E.;			
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CC	CC	RA	RT Down syndrome"; PubMed=9226371;			
CC	CC	RA	RT MEDLINE=97139930; PubMed=9226371;			
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CC	CC	RA	RT "Cloning of a novel human neural cell adhesion molecule gene (NCAM2) that maps to chromosome region 21q21 and is potentially involved in Paoloni-Giacobino A., Chen H., Antonarakis S.E.;			
CC	CC	RA	RT Down syndrome"; PubMed=9226371;			
CC	CC	RA	RT MEDLINE=97139930; PubMed=9226371;			
CC	CC	RA	RT PAOLONI-GIACOBINO A., CHEN H., ANTONARAKIS S.E.;			
CC	CC	RA	RT "Cloning of a novel human neural cell adhesion molecule gene (NCAM2) that maps to chromosome region 21q21 and is potentially involved in Paoloni-Giacobino A., Chen H., Antonarakis S.E.;			
CC	CC	RA	RT Down syndrome"; PubMed=9226371;			
CC	CC	RA	RT MEDLINE=97139930; PubMed=9226371;			
CC	CC	RA	RT PAOLONI-GIACOBINO A., CHEN H., ANTONARAKIS S.E.;			
CC	CC	RA	RT "Cloning of a novel human neural cell adhesion molecule gene (NCAM2) that maps to chromosome region 21q21 and is potentially involved in Paoloni-Giacobino A., Chen H., Antonarakis S.E.;			
CC	CC	RA	RT Down syndrome"; PubMed=9226371;			
CC	CC	RA	RT MEDLINE=97139930; PubMed=9226371;			
CC	CC	RA	RT PAOLONI-GIACOBINO A., CHEN H., ANTONARAKIS S.E.;			
CC	CC	RA	RT "Cloning of a novel human neural cell adhesion molecule gene (NCAM2) that maps to chromosome region 21q21 and is potentially involved in Paoloni-Giacobino A., Chen H., Antonarakis S.E.;			
CC	CC	RA	RT Down syndrome"; PubMed=9226371;			
CC	CC	RA	RT MEDLINE=97139930; PubMed=9226371;			
CC	CC	RA	RT PAOLONI-GIACOBINO A., CHEN H., ANTONARAKIS S.E.;			
CC	CC	RA	RT "Cloning of a novel human neural cell adhesion molecule gene (NCAM2) that maps to chromosome region 21q21 and is potentially involved in Paoloni-Giacobino A., Chen			

DR	InterPro; IPR007110; Ig-like.	OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
DR	InterPro; IPR003598; Ig_C2.	OC	Gallus.
DR	InterPro; IPR003006; Ig_MHC.	NCBI TaxID=9031;	NCBI TaxID=9031;
DR	Pfam; PF00041; fn3 ; 2.	OX	RN [1]
DR	Pfam; PE00047; ig; 5.	RP	SEQUENCE FROM N.A.
SMART	SM00060; FN3 ; 2.	RC	TISSUE=Embryonic brain;
DR	SMART; SM00408; IgC2 ; 5.	RX	MEDLINE=91271300; PubMed=1711213;
PROSITE	PS50835; IG_LIKE ; 5.	RA	Chou Y.-H.; Hayman M.J.;
DR	Cell adhesion; Transmembrane; Glycoprotein; Repeat;	RT	"Characterization of a member of the immunoglobulin gene superfamily that possibly represents an additional class of growth factor receptor."
KW	Immunoglobulin domain; Signal.	RT	RT
FT	SIGNAL ; 1	RT	RT
FT	CHAIN ; 20	RL	Proc. Natl. Acad. Sci. U.S.A. 88:4897-4901(1991).
FT	DOMAIN ; 20	CC	- - FUNCTION: MAY FUNCTION AS A CELL ADHESION MOLECULE. LACKS PROBABLY THE CATALYTIC ACTIVITY OF TYROSINE KINASE.
FT	TRANSMEM	CC	- - SUBCELLULAR LOCATION: Type I membrane protein.
FT	DOMAIN ; 698	CC	- - TISSUE SPECIFICITY: EXPRESSED IN BONE MARROW, SPLEEN, BURSA, THYMUS AND BRAIN. WEAKLY EXPRESSED IN FIBROBLASTS ALSO EXPRESSED IN EMBRYONIC LIVER.
FT	DOMAIN ; 719	CC	- - SIMILARITY: Contains 7 immunoglobulin-like C2-type domains.
FT	DOMAIN ; 21	CC	- - SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. INSULIN RECEPTOR SUBFAMILY.
FT	DOMAIN ; 108	CC	-----
FT	DOMAIN ; 113	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
FT	DOMAIN ; 208	CC	-----
FT	DOMAIN ; 302	CC	-----
FT	DOMAIN ; 401	CC	-----
FT	DOMAIN ; 482	CC	-----
FT	DOMAIN ; 594	CC	-----
FT	DISULFID ; 42	CC	-----
FT	DISULFID ; 136	CC	-----
FT	DISULFID ; 232	CC	-----
FT	DISULFID ; 322	CC	-----
FT	DISULFID ; 422	CC	-----
FT	CARBODY ; 177	CC	-----
FT	CARBODY ; 219	CC	-----
FT	CARBODY ; 309	CC	-----
FT	CARBODY ; 406	CC	-----
FT	CARBODY ; 419	CC	-----
FT	CARBODY ; 445	CC	-----
FT	CARBODY ; 474	CC	-----
FT	CARBODY ; 562	CC	-----
SQ	SEQUENCE ; 837 AA;	CC	-----
SQ	92932 MW;	CC	-----
SQ	C3D03410665741C1 CRC64;	CC	-----
Query Match	Best Local Similarity	10.1%	Score 165; DB 1; Length 837;
Matches	72; Conservative	24.3%	Pred. No. 3.9e-06; Gaps 15;
Qy	44 QPF--ESVELSCITIDSQTSDPPIEWKIQDEQTTVYFFDNKIQGDLAGPAEILGKTSI	100	DR Pfam; PF00069; Pkinase; 1.
Db	124 QEFKQGEDAEVVCRVSSSPA--PAVSMLYHNBEVT--ISDN----RLAMLNNL	171	DR PRINTS; PR00109; TYRKINSE.
Qy	101 KIWNVTPRDSALYRCE--VVANRDRKEIDELVIETLVQVKRPTVCPYKAVPV---	152	DR ProdDom; PD000001; Prot_kinase; 1.
Db	172 QILINKNSDEGYRCERARGE----IDFRDIVVYNPAPMSMPXSFN	219	DR Receptor; Transmembrane_Signal; Glycoprotein; Cell adhesion; SMART; SM00408; IgC2; 1.
Qy	153 ----GRMATLHQQESBGGHPRPHYSWYNDVPLPTDSRANPRFNSHNSSETGTIVFT	207	DR PROSITE; PS50835; Ig_Like; 7.
Db	220 ATAERGEMTFSCRAS-GSPEPAISWRNGKLIE-----ENEKYLKGSNTTELTVR	269	DR DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Qy	208 AVHKDSDGQYYCIALSNDGARSARQEEMEVYDNLNIGGIIGEVVLWAVLALITLGICCA	267	DR DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
Db	270 NIINSDGPPYCRAKTAG---EDEKQAF-----LQVFVQPHIOLKNETY	313	DR KW Immunoglobulin domain; Repeat.
Qy	268 ERGYFINKQDGEYSYKPNPKGP-----DGVNVTTRTDDEGDFR----HKSS	307	DR FT SIGNAL ; 1
Db	314 ENQQ-VTLVCDAB-----GEPipeITWRAVGDGFTEGDKSPDGRIEVKQHGSS	363	DR FT CHAIN ; 23
RESULT 15	PTK7 CHICK	STANDARD;	PRT; 1051 AA.
ID	PTK7 CHICK	STANDARD;	PRT; 1051 AA.
AC	Q91078;	FT DISULFID	137
DT	30-MAY-2000 (Rel. 39, Created)	FT DISULFID	187
DT	30-MAY-2000 (Rel. 39, Last sequence update)	FT DISULFID	282
DT	15-SEP-2003 (Rel. 42, Last annotation update)	FT DISULFID	326
DE	Tyrosine-protein kinase-like 7 precursor (Kinase like protein).	FT DISULFID	372
GN	PTK7 OR KLG	FT DISULFID	462
OS	Gallus gallus (Chicken)	FT DISULFID	505
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	FT DISULFID	551
OC	N-LINKED (GLCNAC. . .)	FT DISULFID	645
OC	(POTENTIAL)	FT CARBOHYD	103
OC	N-LINKED (GLCNAC. . .)	FT CARBOHYD	202
OC	(POTENTIAL)	FT CARBOHYD	255
OC	N-LINKED (GLCNAC. . .)	FT CARBOHYD	264

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PT CARBOHYD    444      444      N-LINKED (GLCNAC. .) (POTENTIAL).
PT CARBOHYD    548      548      N-LINKED (GLCNAC. .) (POTENTIAL).
PT CARBOHYD    627      627      N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 1051 AA; 116366 MW; 175244AEE4CB702 CRC64;
Query Match 10.1%; Score 164.5; DB 1; Length 1051;
Best Local Similarity 24.5%; Pred. No. 5.6e-06;
Matches 66; Conservative 35; Mismatches 109; Indels 59; Gaps 11;
Qy 40 TPVVOQFESVE----LSCITDSQTSDPRLEKKIQLDEOTTYFFDNKIQGDLAGRAE 93
Db 486 TPPPOPIQCMEFNKEYTVSCSATGRE-KPTLQWTID-----GSSLPHYSHRAG 534
Qy 94 ILGKTSLIKWNTRROSALYCEVVARNDRKREIDEIVELTVQVKRPVTVCRVPAVPG 153
Db 535 I-----LSFKYVSRSDDGGNYTC-IASNPSQGEIRATVQLVAVYVTFKLEPEPTVYQG 587
Qy 154 KMATLHCQESEGHRPHRPHYSWYRNNDVPLPLTDSRANPRFRNSSHLNSETGTLLVFTAVHKDD 213
Db 588 HTAMFQQ-AEGDPVPHIQWKGRDKIL-DPSKLPLQIMDN-----GSIVIYDTTED 639
Qy 214 SGQYYCIAANDAG-----SARCEEQE-----MEYVDLNGGIIGGVLV 251
Db 640 SCKYTCTAGNSCNIKHREAFLYVVDKPAEEDEGPSSHTPYKMIQITGSLSGAAVAYII 699
Qy 252 VIALVALITLGICCAVRRGYFINNKQDG 280
Db 700 VLGIMF-----YCKKRKAKRLKKHDE 723

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Search completed: December 15, 2003, 14:52:33
 Job time : 20 secs